

US 6,492,106 B1

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 15

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus rattus
- (G) CELL TYPE: pheochromocytoma
- (H) CELL LINE: PC12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGCG GCACGAGCG GTAGCTGAGG CGGTGGCCGA AGCCCCGCCA ACCTCAGGGC	60
AAGATGCTTG GGACAGGCC TGCCACGCC ACCGCCGGTG CCGCCACATC TAGCAACGTG	120
AGCGTTCTGC AGCAGTTCGC CAGTGGCTG AAGAGCCGA ATGAGGAGAC CAGGGCCAAA	180
GCAGCCAAGG AGCTCCAGCA CTATGTCACC ATGGAACITTC GAGAGATGAG TCAGGAGGAG	240
TCTACTCGCT TCTATGACCA GCTGAACCAT CACATTTTG AACTGGTTTC CAGCTCAGAC	300
GCCAATGAGA GGAAGGGTGG CATCTGGCC ATTGCCAGCC TCATTGGAGT GGAAGGTGG	360
AATTCCACCA GGATTGGCAG ATTTGCAAC TACCTTCGGA ACCTCCCTCC CTCAAGTGAT	420
CCAGTTGTCA TGGAGATGGC ATCCAAGGCC ATTGGCCGCC TTGCAATGGC AGGGGACACT	480
TTCACTGCTG AGTATGTGGA GTTTGAAGTC AAGCGAGCCT TGGAGTGGCT GGGTGCTGAC	540
CGAAATGAGG GCCGGAGACA TGCAGCTGTC CTCGTTCTCC TGAGCTGGC CATCAGCGTC	600
CCCACCTCTCT TCTTCCAGCA AGTTCAAGCC TTCTTGACA ACATTTTGT GGCTGTGTGG	660
GACCCCAAGC AGGCCATCCG TGAAGGAGCT GTGGCTGCC TTCGTGCCTG TCTGATTCTT	720
ACCACGCAGC GGGAGCCGAA GGAGATGCAG AAGCCTCAGT GGTACAGGCA CACATTGAA	780
GAAGCAGAGA AAGGTTTGA TGAGACCTG GCCAAAGAGA AGGGTATGAA CCGAGATGAT	840
CGAATCCACG GGGCTTGCT GATCCTCAAC GAGCTCGTCC GAATCAGCAG CATGGAGGG	900
GAGCGTCTGA GAGAGGAGAT GGAGGAAATC ACCCAGCAGC AGCTGGTACA TGACAAGTAC	960
TGCAAAGACC TAATGGGCTT TGGGACAAAG CCTCGGCACA TCACTCCCTT CACCAGCTTC	1020
CAGGCTGTGC AGCCCCAGCA GTCAAACGCC TTGGTGGAC TGCTGGGTA CAGCTCCAC	1080
CAAGGCTAA TGGGGTTTGG GGCTTCCCCC AGCCCTACAA AGTCCACTCT GGTGGAAAGC	1140
CGTTGTTGCA GAGACTTGAT GGAAGAGAAA TTTGATCAGG TGTGCCAGTG GGTGCTGAAA	1200
TCTAGGAGCA GCAAGAACTC ACTGATCCAA ATGACAATCC TTAATCTGTT GCCCCCTTG	1260
GTTGCATTC GACCGTCTGC CTTCACAGAT ACCCAGTACCG TGCAAGACAC CATGAACCAT	1320
GTCCTGAGCT GTGTCAAGAA GGAAAAGGAA CGGACCGCAG CGTTCAGGC CCTAGGGCTG	1380
CTTTCTGTGG CGGTGAGGTC CGAGTTAAC GTCTACCTGC CCCGAGTACT TGACATCATC	1440
CGAGCAGCCC TGCCTCCAAA GGACTTTGCC CACAAGAGGC AGAAAAGTGT GCAGGTGGAT	1500

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GCCACAGTGT TCACGTGCAT CAGCATGCTG GCGCGGGCCA TGGGGCAGG CATCCAGCAG	1560
GACATCAAGG AGCTGCTGGA GCCCCATGTTG GCAGTGGGCC TGAGCCCTGC GCTCACTGCT	1620
GTGCTCTATG ACCTGAGCCG GCAGATTCCG CAGCTGAAGA AAGATATTCA GGACGGGCTT	1680
CTGAAGATGC TGTCCCCTGGT CCTTATGCAC AAACCCCTGC GGCACCCGGG CATGCCAAA	1740
GGCCTGGCCC ACCAGCTGGC CTCCCCAGGT CTTACCACCC TCCCTGAGGC CAGCGACGTG	1800
GCCAGCATCA CTCTTGCCCT TCGAACTCTC GGCAGCTTIG AATTGAAGG CCACTCTCTG	1860
ACCCAGTTCG TCCGACACTG CGCAGATCAT TTCCCTGAACA GTGAGCACAA GGAGATCCGC	1920
ATGGAAGCAG CCCGCACCTG CTCCCGCTG CTCACACCCCT CCATCCACCT CATCAGCGC	1980
CATGCCCATG TGGTTAGCCA GACCGCACTG CAAGTGGTAG CAGATGTGCT CAGCAAGCTG	2040
CTTGTGGTCG GCATAAACAGA TCCCTGATCCT GATATCCGCT ACTGTGTCTT GGCCTCCCTG	2100
GATGAGCGCT TCGATGCCCA CCTTGGCCAG GCAGAAAATC TACAAGCTCT GTTTGTGGCT	2160
CTGAATGACC AGGTCTTGA GATCCGAGAG CTGGCCATCT GCACTGTGGG CCGACTCAGT	2220
AGCATGAACC CAGCCTTGT CATGCCTTTC CTGCGCAAGA TGCTCATCCA GATTTTGACA	2280
GAGCTGGAGC ACAGTGGCAT TGGGAGAAC AAGGAGCAGA GTGCCCGCAT GCTGGGGCAC	2340
CTGGTCTCCA ATGCCCTCCG CCTCATCCGC CCCTATATGG AGCCTATTCT GAAGGCTTTA	2400
ATTTTGAAC TCAAAGATCC AGACCCGTAC CCAAACCCGG GCGTGATCAA TAACGTGTTG	2460
GCCACTATAG GAGAACTGGC TCAGGTTAGC GGCCTGGAGA TGAGGAAGTG GGTGGACGAG	2520
CTCTTTGTCA TCATCATGGA CATGCTGCAG GACTCCTCTC TTCTGGCCAA AAGACAGGTG	2580
GCTTTGTGGA CCCTGGGACA GTTGGTGGCC AGTACTGGCT ACGTGGTGGA GCCCTACAGG	2640
AAGTACCCCA CTCTGCTTGA AGTGCTGCTG AATTTCTGA AGACGGAGCA GAACCAGGGC	2700
ACTCGGAGAG AGGCCATCCG AGTGTGTTAGGG CTCCCTGGGG CTTTGGACCC CTACAAGCAC	2760
AAAGTGAACA TCGGCATGAT TGACCACTGCC CGAGATGCTT CTGCTGTCAG CCTGTCAGAA	2820
TCCAAGTCAA GTCAAGATTC CTCTGACTAC AGCACCAGTG AAATGCTGGT CAACATGGGA	2880
AACCTGCCAC TGGACGAGTT CTACCCCGCC GTGTCCATGG TGGCTTGAT GCGGATCTTC	2940
CGAGACCAGT CCCTCTCTCA CCACCAACACC ATGGTGGTTC AGGCCATCAC CTTCATCTTC	3000
AAGTCCCTGG GGCTCAAGTG TGTGCAGTTC CTGCCCGAGG TCATGCCAC GTTCCCTAAC	3060
GTCATCCGAG TCTGTGATGG GCCCATCCGG GAATTTCTGT TCCAGCAGCT GGGAAATGCTG	3120
GTGTCCTTTC TGAAGAGGCCA CATCCGTCCC TACATGGATG AAATAGTCAC CCTCATGAGA	3180
GAATTTGGG TCATGAACAC CTCATCCAG AGCACAATCA TTCTCTCAT TGAGCAAATC	3240
GTGGTGGCTC TTGGGAGGTGA ATTAAAGCTC TACCTGCCCT AGCTGATCCC ACACATGCTG	3300
CGTGTCTTCA TGCGATGACAA CAGCCAGGGC CGCATAGTCT CCATCAAGCT GTTAGCAGCG	3360
ATCCAGCTGT TTGGGCCAA CCTGGATGAC TATCTGCACT TGTGTTGCC TCCGATCGTG	3420
AAATTGTTTG ATGCCCTGTA AGTTCCACTG CCGTCGAGAA AGGCAGCGTT GGAGACAGTG	3480
GACCGCCTGA CAGAGTCCCT GGATTTCACT GACTATGCCCT CCCGCATCAT TCACCCGATT	3540
GTTCGCACGC TAGACCAGAG CCCAGAGCTG CGCTCCACAG CCATGGACAC CCTGTCCTCA	3600
CTTGTGTTTC AACTAGGGAA GAAGTACCAAG ATCTTCATTC CAATGGTGA TAAAGTCCTT	3660
GTGGGACACC GGATCAATCA CCAGCGCTAC GACGTGCTGA TCTGCAGAAT CGTCAAGGGG	3720
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AGCCAGGGAG ATGCCCTGGC CAGTGGACCA GTTGAAACAG GACCCATGAA GAAACTGCAT	3840
GTCAGCACCA TCAACCTCCA AAAGGCCCTGG GGAGCTGCCA GAAGGGTCTC CAAGGACGAC	3900

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TGGCTGGAGT GGCTGCGACG CTTGAGTC TGAGCTGCTGA AGGATTCCCTC ATCACCTTCC	3960
CTGGCGCTCAT GCTGGGCCCT GGCCCAGGCC TACAACCCA TGGCCAGGGA TCTCTTCAC	4020
GCTGCGTTTG TGTCTGCTG GTCTGAAC TG AATGAAGACC AACAAAGATGA GCTCATCAGG	4080
AGCATTGAGT TGGCTCTCAC TTCTCAAGAC ATTGCTGAAG TCACACAAAC CCTCTTGAAAC	4140
TTGGCTGAGT TCATGGAGCA CAGTGACAAG GGCCCCCTAC CACTGAGAGA TGACAATGGC	4200
ATCGTGCCTGT TGGGTGAGAG AGCTGCAAAG TGCCGGGCAT ATGCCAAAGC ACTACACTAC	4260
AAAGAGCTGG AGTTCCAGAA GGGGCCACG CCTGCCATAC TTGAGTCCCT CATCAGCATT	4320
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TTCGGAGAGC TGGGAGATCCA GGCCACCTGG TATGAGAAGT TGCATGAGTG GGAGGACGCC	4440
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AAAGTGGACTC TGGTTAATGA CGAGACCCAG GCTAAGATGG CCCGGATGGC TGCTGCAGCA	4620
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ACTCACGATG GAGCATTCTA CAGAGCAGTG TTGGCACTGC ATCAGGATCT CTTCTCCTTG	4740
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CGGTCCCTTG TGGTCAGCCC TCACGAGGAC ATGAGAACCT GGCTCAAGTA CGCAAGCCTG	5040
TGTGGCAAGA GCGGCAGACT GGCTCTTGCT CATAAAACCT TAGTGTGCT CTTGGGAGTT	5100
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AAGCAGGAGC TGCATAAGCT CATGGCAGG TGTGTTCTGA AACTTGGGA GTGGCAGCTG	5340
AACTTCCAGG GCATCAACGA GAGCACCAC CCAAAGGTGC TACAGTACTA CAGTGCCTG	5400
ACAGAGCATG ACCGCAGCTG GTATAAGGCT TGGCACCGAT GGGCAGTGAT GAACTTGAA	5460
GCCGTGCTAC ACTACAAACA TCAGAACCAA GCCCCGGATG AGAAGAAGAA ACTGCCCAT	5520
GCCAGCGGG CCAACATCAC CAATGCCACC ACCACTGCCA CCACCGCTGC CTCCGCTGCC	5580
GCTGCCACCA GCACAGAGGG CAGCAACAGT GAAAGTGAAG CCGAGAGCAA TGAGAGCAGC	5640
CCCACCCCGT CCCCTCTGCA GAAGAAGGTC ACTGAGGATT TGTCCAAAC CCTCTTGTG	5700
TACACTGTCC CTGCTGTCCA AGGCTCTTC CGTTCTATCT CCTTGTGAG AGCAACAAAC	5760
CTCCAGGATA CACTCAGAGT CCTCACCTTG TGGTTGATT ATGGTCACTG GCCAGATGTC	5820
AATGAAGGCC TGGTGGAGG GGTGAAGGCC ATACAGATTG ACACCTGGTT ACAGGTTATA	5880
CCTCAGCTCA TTGCAAGAAT TGACACGCC AGACCCCTGG TGGCCGGCT CATTCAACAG	5940
CTCCTCACAG ATATTGGTCG GTACCACCCA CAGGCCCTCA TCTACCCCT GACGGTGGCT	6000
TCTAAGTCTA CCACACAGC CCGTCACAAT GCAGCCAACA AGATCCTGAA GAACATGTGC	6060
GAGCACAGCA ACACGCTAGT ACAGCAGGCC ATGATGGTGA GTGAAGAGCT GATTGAGTA	6120
GCCATCCTCT GGCATGAGAT GTGGCATGAA GGCCTAGAG AGGCCTCTCG CTTGTACTTT	6180
GGGGAGAGGA ACGTCAAAGG CATGTTGAG GTGCTGGAGC CCCTGCATGC TATGATGGAA	6240

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CGCGGTCCCC AGACCCGTAA GGAAACGTCC TTTAATCAGG CATATGGTCG AGATTAATG	6300
GAGGCACAAG AATGGTCCG AAAGTACATG AAATCAGGGA ACGTCAAGGA CCTCACCCAA	6360
GCCTGGGACC TCTACTATCA CGTGTTCA CGGATCTCCA AGCAGCTACC ACAGCTCAC	6420
TCCCTGGAGC TGCAGTATGT GTCCCCAAA CTTTTGATGT GCAGAGACCT TGAATTGGCT	6480
GTGCCAGGAA CATATGACCC CAACCAGACA ATCATTGCA TTCAGTCCAT AGCCCCGTCT	6540
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CACGAGTTG TTTTCCCTCT GAAAGGCCAT GAAGATCTGC GGCAGGACGA GCGAGTGATG	6660
CAGCTCTTG GCCTGGTAA CACACTCCTA GCCAATGACC CAACTTCTCT TCGAAAGAAC	6720
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GTGCCCCACT GTGACACGCT GCATGCCCTC ATCCGGACT ACAGAGAGAA GAAGAAGATC	6840
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GCCAAGCTGC TGTGGCTGAA AAGCCCCAGC TCAGAGGTGT GTTTGACCG AAGAACCAAT	7020
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CACCCATCCA ACCTGATGCT GGACCGGCTG AGTGGAAAGA TCCTGCACAT TGACTTTGGG	7140
GACTGCTTTG AGGTTGCTAT GACCAGAGG AAATTTCCAG AAAAGATTCC ATTAGACTA	7200
ACAAGAATGT TGACCAATGC TATGGAGGTT ACCGGTCTCG ATCGCAACTA TAGAACACAA	7260
TGCCACACAG TGATGGAGGT GCTTCGGGAG CACAAGGACA GTGTCATGGC TGTGCTAGAA	7320
GCCTTTGTCT ATGACCCCTCT GCTGAATTGG AGGCTGATGG ACACAAATGC CAAAGCAAC	7380
AACCGGTCCC GAACCAGGAC AGACTCCTAT TCTGCAGGCC ATGCACTAGA AATTTGGAC	7440
GGTGTAGAAC TTGGAGAAC AGCCCTAAAG AAAACAGGGA CCACGTGCCC AGAATCCATC	7500
CATTCTTCA TTGGAGATGG TTTGGTAAA CCAGAAGCCT TAAACAAGAA AGCTATTCA	7560
ATTATTAACA GGTTCCAGA TAAGCTCACT GGTCGGGATT TCTCTCATGA TGACACTTTG	7620
GATGTTCCAA CCCAAGTGGAA ACTGCTTATC AAGCAAGCGA CATCTCATGA GAACCTCTGC	7680
CAGTGCCTACA TTGGCTGGTGC TCCCTCTGG TAAACCAAGGC CTGGCAAAAGA AAATCATCTC	7740
CTCCGATGCT TTTGTACCTT GGTCTGTGCT TCCAGTGGAC TGAAACCATG GTCATAAAAGT	7800
TGGACTTTGT TAATATTTCG AAATGTATAT GAAAAGAACT ACTGTATATT CAAAGTTGGC	7860
TTATGCCAAC CTCTTAGCTG CTGTTGAAAA GACACTGTCA GAAACACAAG GCTTGATTCA	7920
GTTCAGGAGA CAGTGAACAA CAGTAATCCT ACAGAAACCA AGCCTTTGAT TTTGGAGAA	7980
CAGAAGATGA GTAAGTCACT AAGAAATACG GGTTTGACT TAACTTACAG AAGAACTCAT	8040
CATACGCTT TGCTGACCGA ATAATCTAGT TGATCCCTC AACCAAGGGC TTCAACAGCA	8100
AGGACACAGA TGTCAAGCACT CCACCATCCT GTTACCTCAG CCGTCCCTGG ATGCAGTGGC	8160
AACATCTGCA GGATGGGCCA CCGTGTGTGT AAGAAGATCT GTCTTCCACC TGATCCCATG	8220
ATGCTGAACC TCACAGAGCC GGCTTCCAG GAAGGACGTT TGCTCAGACG CCTGGCCACC	8280
GAGGATGAGC AGGTGTGCCA GGATCTCACT GCAGGGTCCA CGCTGGCCCT GCTGCTGTGT	8340
TCAGTGAGGG ATGGATATGT TGTGTTGCA GCAGGGACTC AGAACACAAA TGCTTTGTG	8400
GAAGTGTGA TCTCAGAGGG ACACTAGCGC AGGTTGTGAA TTAAGAGCAA AGTAATATC	8460
CAACTAAACA CAAAGTATAA GTGAAGCCAC ATCTAGACAC CATTGTATCT GAGTAATTTC	8520
TGTGCCAATA AATGACATCA GAATTTAAA AGTAAAAAAA ACGATATCAA GCTTATCGAT	8580
ACCGTCGACC TCGAGGGG	8598

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2549 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus rattus
- (F) TISSUE TYPE: pheochromocytoma
- (G) CELL TYPE: PC12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Gly	Thr	Gly	Pro	Ala	Thr	Ala	Gly	Ala	Ala	Thr	Ser
1													
													15

Ser	Asn	Val	Ser	Val	Leu	Gln	Gln	Phe	Ala	Ser	Gly	Leu	Lys	Ser	Arg
															30
20															

Asn	Glu	Glu	Thr	Arg	Ala	Lys	Ala	Ala	Lys	Glu	Leu	Gln	His	Tyr	Val
															45
35															

Thr	Met	Glu	Leu	Arg	Glu	Met	Ser	Gln	Glu	Glu	Ser	Thr	Arg	Phe	Tyr
															50
50															

Asp	Gln	Leu	Asn	His	His	Ile	Phe	Glu	Leu	Val	Ser	Ser	Ser	Asp	Ala
															60
65															

Asn	Glu	Arg	Lys	Gly	Gly	Ile	Leu	Ala	Ile	Ala	Ser	Leu	Ile	Gly	Val
															95
85															

Glu	Gly	Gly	Asn	Ser	Thr	Arg	Ile	Gly	Arg	Phe	Ala	Asn	Tyr	Leu	Arg
															100
100															

Asn	Leu	Leu	Pro	Ser	Ser	Asp	Pro	Val	Val	Met	Glu	Met	Ala	Ser	Lys
															115
115															

Ala	Ile	Gly	Arg	Leu	Ala	Met	Ala	Gly	Asp	Thr	Phe	Thr	Ala	Glu	Tyr
															130
130															

Val	Glu	Phe	Glu	Val	Lys	Arg	Ala	Leu	Glu	Trp	Leu	Gly	Ala	Asp	Arg
															145
145															

Asn	Glu	Gly	Arg	Arg	His	Ala	Ala	Val	Leu	Val	Leu	Arg	Glu	Leu	Ala
															165
165															

Ile	Ser	Val	Pro	Thr	Phe	Phe	Gln	Gln	Val	Gln	Pro	Phe	Phe	Asp	
															180
180															

Asn	Ile	Phe	Val	Ala	Val	Trp	Asp	Pro	Lys	Gln	Ala	Ile	Arg	Glu	Gly
															195
195															

Ala	Val	Ala	Ala	Leu	Arg	Ala	Cys	Leu	Ile	Leu	Thr	Thr	Gln	Arg	Glu
															210
210															

Pro	Lys	Glu	Met	Gln	Lys	Pro	Gln	Trp	Tyr	Arg	His	Thr	Phe	Glu	Gl
															225
225															

Ala	Glu	Lys	Gly	Phe	Asp	Glu	Thr	Leu	Ala	Lys	Glu	Lys	Gly	Met	Asn
															245
245															

Arg	Asp	Asp	Arg	Ile	His	Gly	Ala	Leu	Leu	Ile	Leu	Asn	Glu	Leu	Val
															260
260															

Arg	Ile	Ser	Ser	Met	Glu	Gly	Glu	Arg	Leu	Arg	Glu	Glu	Met	Glu	Glu
															275
275															

Ile	Thr	Gln	Gln	Gln	Leu	Val	His	Asp	Lys	Tyr	Cys	Lys	Asp	Leu	Met
															290
290															

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Gly Phe Gly Thr Lys Pro Arg His Ile Thr Pro Phe Thr Ser Phe Gln  
305                   310                   315                   320

Ala Val Gln Pro Gln Gln Ser Asn Ala Leu Val Gly Leu Leu Gly Tyr  
325                   325                   330                   335

Ser Ser His Gln Gly Leu Met Gly Phe Gly Ala Ser Pro Ser Pro Thr  
340                   345                   345                   350

Lys Ser Thr Leu Val Glu Ser Arg Cys Cys Arg Asp Leu Met Glu Glu  
355                   360                   365

Lys Phe Asp Gln Val Cys Gln Trp Val Leu Lys Cys Arg Ser Ser Lys  
370                   375                   380

Asn Ser Leu Ile Gln Met Thr Ile Leu Asn Leu Leu Pro Arg Leu Val  
385                   390                   395                   400

Ala Phe Arg Pro Ser Ala Phe Thr Asp Thr Gln Tyr Leu Gln Asp Thr  
405                   410                   415

Met Asn His Val Leu Ser Cys Val Lys Lys Glu Lys Glu Arg Thr Ala  
420                   425                   430

Ala Phe Gln Ala Leu Gly Leu Leu Ser Val Ala Val Arg Ser Glu Phe  
435                   440                   445

Lys Val Tyr Leu Pro Arg Val Leu Asp Ile Ile Arg Ala Ala Leu Pro  
450                   455                   460

Pro Lys Asp Phe Ala His Lys Arg Gln Lys Thr Val Gln Val Asp Ala  
465                   470                   475                   480

Thr Val Phe Thr Cys Ile Ser Met Leu Ala Arg Ala Met Gly Pro Gly  
485                   490                   495

Ile Gln Gln Asp Ile Lys Glu Leu Leu Glu Pro Met Leu Ala Val Gly  
500                   505                   510

Leu Ser Pro Ala Leu Thr Ala Val Leu Tyr Asp Leu Ser Arg Gln Ile  
515                   520                   525

Pro Gln Leu Lys Asp Ile Gln Asp Gly Leu Leu Lys Met Leu Ser  
530                   535                   540

Leu Val Leu Met His Lys Pro Leu Arg His Pro Gly Met Pro Lys Gly  
545                   550                   555                   560

Leu Ala His Gln Leu Ala Ser Pro Gly Leu Thr Thr Leu Pro Glu Ala  
565                   570                   575

Ser Asp Val Ala Ser Ile Thr Leu Ala Leu Arg Thr Leu Gly Ser Phe  
580                   585                   590

Glu Phe Glu Gly His Ser Leu Thr Gln Phe Val Arg His Cys Ala Asp  
595                   600                   605

His Phe Leu Asn Ser Glu His Lys Glu Ile Arg Met Glu Ala Ala Arg  
610                   615                   620

Thr Cys Ser Arg Leu Leu Thr Pro Ser Ile His Leu Ile Ser Gly His  
625                   630                   635                   640

Ala His Val Val Ser Gln Thr Ala Val Gln Val Val Ala Asp Val Leu  
645                   650                   655

Ser Lys Leu Leu Val Val Gly Ile Thr Asp Pro Asp Pro Asp Ile Arg  
660                   665                   670

Tyr Cys Val Leu Ala Ser Leu Asp Glu Arg Phe Asp Ala His Leu Ala  
675                   680                   685

Gln Ala Glu Asn Leu Gln Ala Leu Phe Val Ala Leu Asn Asp Gln Val  
690                   695                   700

Phe Glu Ile Arg Glu Leu Ala Ile Cys Thr Val Gly Arg Leu Ser Ser  
705                   710                   715                   720

Met Asn Pro Ala Phe Val Met Pro Phe Leu Arg Lys Met Leu Ile Gln

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725	730	735
Ile Leu Thr Glu Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln		
740	745	750
Ser Ala Arg Met Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile		
755	760	765
Arg Pro Tyr Met Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys		
770	775	780
Asp Pro Asp Pro Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala		
785	790	795
800		
Thr Ile Gly Glu Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp		
805	810	815
Val Asp Glu Leu Phe Val Ile Ile Met Asp Met Leu Gln Asp Ser Ser		
820	825	830
Leu Leu Ala Lys Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val		
835	840	845
Ala Ser Thr Gly Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu		
850	855	860
Leu Glu Val Leu Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr		
865	870	875
880		
Arg Arg Glu Ala Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro		
885	890	895
Tyr Lys His Lys Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala		
900	905	910
Ser Ala Val Ser Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp		
915	920	925
Tyr Ser Thr Ser Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp		
930	935	940
Glu Phe Tyr Pro Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg		
945	950	955
960		
Asp Gln Ser Leu Ser His His Thr Met Val Val Gln Ala Ile Thr		
965	970	975
Phe Ile Phe Lys Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln		
980	985	990
Val Met Pro Thr Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile		
995	1000	1005
Arg Glu Phe Leu Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys		
1010	1015	1020
Ser His Ile Arg Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu		
1025	1030	1035
1040		
Phe Trp Val Met Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile		
1045	1050	1055
Glu Gln Ile Val Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro		
1060	1065	1070
Gln Leu Ile Pro His Met Leu Arg Val Phe Met His Asp Asn Ser Gln		
1075	1080	1085
Gly Arg Ile Val Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly		
1090	1095	1100
Ala Asn Leu Asp Asp Tyr Leu His Leu Leu Pro Pro Ile Val Lys		
1105	1110	1115
1120		
Leu Phe Asp Ala Pro Glu Val Pro Leu Pro Ser Arg Lys Ala Ala Leu		
1125	1130	1135
Glu Thr Val Asp Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala		
1140	1145	1150

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Ser Arg Ile Ile His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu  
 1155 1160 1165

Leu Arg Ser Thr Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu  
 1170 1175 1180

Gly Lys Lys Tyr Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val  
 1185 1190 1195 1200

Arg His Arg Ile Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile  
 1205 1210 1215

Val Lys Gly Tyr Thr Leu Ala Asp Glu Glu Asp Pro Leu Ile Tyr  
 1220 1225 1230

Gln His Arg Met Leu Arg Ser Ser Gln Gly Asp Ala Leu Ala Ser Gly  
 1235 1240 1245

Pro Val Glu Thr Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn  
 1250 1255 1260

Leu Gln Lys Ala Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp  
 1265 1270 1275 1280

Leu Glu Trp Leu Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser  
 1285 1290 1295

Ser Pro Ser Leu Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro  
 1300 1305 1310

Met Ala Arg Asp Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu  
 1315 1320 1325

Leu Asn Glu Asp Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala  
 1330 1335 1340

Leu Thr Ser Gln Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu  
 1345 1350 1355 1360

Ala Glu Phe Met Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp  
 1365 1370 1375

Asp Asn Gly Ile Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala  
 1380 1385 1390

Tyr Ala Lys Ala Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro  
 1395 1400 1405

Thr Pro Ala Ile Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln  
 1410 1415 1420

Gln Pro Glu Ala Ala Ser Gly Val Leu Glu Tyr Ala Met Lys His Phe  
 1425 1430 1435 1440

Gly Glu Leu Glu Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp  
 1445 1450 1455

Glu Asp Ala Leu Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp  
 1460 1465 1470

Asp Pro Glu Leu Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly  
 1475 1480 1485

Glu Trp Gly Gln Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val  
 1490 1495 1500

Asn Asp Glu Thr Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala  
 1505 1510 1515 1520

Trp Gly Leu Gly Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile  
 1525 1530 1535

Pro Arg Asp Thr His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu  
 1540 1545 1550

His Gln Asp Leu Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg  
 1555 1560 1565

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Asp Leu Leu Asp Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser  
1570 1575 1580

Arg Ala Tyr Gly Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu  
1585 1590 1595 1600

Glu Val Ile Gln Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg  
1605 1610 1615

Gln Ile Trp Trp Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp  
1620 1625 1630

Trp Gln Lys Ile Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu  
1635 1640 1645

Asp Met Arg Thr Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly  
1650 1655 1660

Arg Leu Ala Leu Ala His Lys Thr Leu Val Leu Leu Leu Gly Val Asp  
1665 1670 1675 1680

Pro Ser Arg Gln Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val  
1685 1690 1695

Thr Tyr Ala Tyr Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp  
1700 1705 1710

Ala Phe Gln His Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala  
1715 1720 1725

Gln His Ala Ile Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His  
1730 1735 1740

Lys Leu Met Ala Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn  
1745 1750 1755 1760

Leu Gln Gly Ile Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr  
1765 1770 1775

Ser Ala Ala Thr Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala  
1780 1785 1790

Trp Ala Val Met Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn  
1795 1800 1805

Gln Ala Arg Asp Glu Lys Lys Leu Arg His Ala Ser Gly Ala Asn  
1810 1815 1820

Ile Thr Asn Ala Thr Thr Ala Thr Thr Ala Ala Ser Ala Ala Ala  
1825 1830 1835 1840

Ala Thr Ser Thr Glu Gly Ser Asn Ser Glu Ser Ala Glu Ser Asn  
1845 1850 1855

Glu Ser Ser Pro Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp  
1860 1865 1870

Leu Ser Lys Thr Leu Leu Leu Tyr Thr Val Pro Ala Val Gln Gly Phe  
1875 1880 1885

Phe Arg Ser Ile Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu  
1890 1895 1900

Arg Val Leu Thr Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn  
1905 1910 1915 1920

Glu Ala Leu Val Glu Val Lys Ala Ile Gln Ile Asp Thr Trp Leu  
1925 1930 1935

Gln Val Ile Pro Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu  
1940 1945 1950

Val Gly Arg Leu Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His  
1955 1960 1965

Pro Gln Ala Leu Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr  
1970 1975 1980

Thr Ala Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu

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1985	1990	1995	2000
His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu			
2005	2010	2015	
Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu			
2020	2025	2030	
Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe			
2035	2040	2045	
Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr			
2050	2055	2060	
Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu			
2065	2070	2075	2080
Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp			
2085	2090	2095	
Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser			
2100	2105	2110	
Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro			
2115	2120	2125	
Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr			
2130	2135	2140	
Asp Pro Asn Gln Thr Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu			
2145	2150	2155	2160
Gln Val Ile Thr Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly			
2165	2170	2175	
Ser Asn Gly His Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu			
2180	2185	2190	
Arg Gln Asp Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu			
2195	2200	2205	
Leu Ala Asn Asp Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg			
2210	2215	2220	
Tyr Ala Val Ile Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val			
2225	2230	2235	2240
Pro His Cys Asp Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys			
2245	2250	2255	
Lys Lys Ile Leu Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala			
2260	2265	2270	
Pro Asp Tyr Asp His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu			
2275	2280	2285	
His Ala Val Asn Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp			
2290	2295	2300	
Leu Lys Ser Pro Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr			
2305	2310	2315	2320
Thr Arg Ser Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu			
2325	2330	2335	
Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys			
2340	2345	2350	
Ile Leu His Ile Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg			
2355	2360	2365	
Glu Lys Phe Pro Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr			
2370	2375	2380	
Asn Ala Met Glu Val Thr Gly Leu Asp Arg Asn Tyr Arg Thr Thr Cys			
2385	2390	2395	2400
His Thr Val Met Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala			
2405	2410	2415	

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Val Leu Glu Ala Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met  
2420 2425 2430

Asp Thr Asn Ala Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser  
2435 2440 2445

Tyr Ser Ala Gly Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly  
2450 2455 2460

Glu Pro Ala His Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His  
2465 2470 2475 2480

Ser Phe Ile Gly Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys  
2485 2490 2495

Ala Ile Gln Ile Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp  
2500 2505 2510

Phe Ser His Asp Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu  
2515 2520 2525

Ile Lys Gln Ala Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly  
2530 2535 2540

Trp Cys Pro Phe Trp  
2545

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2470 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Pro His Glu Glu Gln Ile Trp Lys Ser Lys Leu Leu Lys Ala  
1 5 10 15

Ala Asn Asn Asp Met Asp Met Asp Arg Asn Val Pro Leu Ala Pro Asn  
20 25 30

Leu Asn Val Asn Met Asn Met Lys Met Asn Ala Ser Arg Asn Gly Asp  
35 40 45

Glu Phe Gly Leu Thr Ser Ser Arg Phe Gly Gly Val Val Ile Gly Ser  
50 55 60

Asn Gly Asp Val Asn Phe Lys Pro Ile Leu Glu Lys Ile Phe Arg Glu  
65 70 75 80

Leu Thr Ser Asp Tyr Lys Glu Glu Arg Lys Leu Ala Ser Ile Ser Leu  
85 90 95

Phe Asp Leu Leu Val Ser Leu Glu His Glu Leu Ser Ile Glu Glu Phe  
100 105 110

Gln Ala Ile Ser Asn Asp Ile Asn Asn Lys Ile Leu Glu Leu Val His  
115 120 125

Thr Lys Lys Thr Asn Thr Arg Val Gly Ala Val Leu Ser Ile Asp Thr  
130 135 140

Leu Ile Ser Phe Tyr Ala Tyr Thr Glu Arg Leu Pro Asn Glu Thr Ser  
145 150 155 160

Arg Leu Ala Gly Tyr Leu Arg Gly Leu Ile Pro Ser Asn Asp Val Glu  
165 170 175

Val Met Arg Leu Ala Ala Lys Thr Leu Gly Lys Leu Ala Val Pro Gly  
180 185 190

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Gly Thr Tyr Thr Ser Asp Phe Val Glu Phe Glu Ile Lys Ser Cys Leu  
195 200 205

Glu Trp Leu Thr Ala Ser Thr Glu Lys Asn Ser Phe Ser Ser Ser Lys  
210 215 220

Pro Asp His Ala Lys His Ala Ala Leu Leu Ile Ile Thr Ala Leu Ala  
225 230 235 240

Glu Asn Cys Pro Tyr Leu Leu Tyr Gln Tyr Leu Asn Ser Ile Leu Asp  
245 250 255

Asn Ile Trp Arg Ala Leu Arg Asp Pro His Leu Val Ile Arg Ile Asp  
260 265 270

Ala Ser Ile Thr Leu Ala Lys Cys Leu Ser Thr Leu Arg Asn Arg Asp  
275 280 285

Pro Gln Leu Thr Ser Gln Trp Val Gln Arg Leu Ala Thr Ser Cys Glu  
290 295 300

Tyr Gly Phe Gln Val Asn Thr Leu Glu Cys Ile His Ala Ser Leu Leu  
305 310 315 320

Val Tyr Lys Glu Ile Leu Phe Leu Lys Asp Pro Phe Leu Asn Gln Val  
325 330 335

Phe Asp Gln Met Cys Leu Asn Cys Ile Ala Tyr Glu Asn His Lys Ala  
340 345 350

Lys Met Ile Arg Glu Lys Ile Tyr Gln Ile Val Pro Leu Leu Ala Ser  
355 360 365

Phe Asn Pro Gln Leu Phe Ala Gly Lys Tyr Leu His Gln Ile Met Asp  
370 375 380

Asn Tyr Leu Glu Ile Leu Thr Asn Ala Pro Ala Lys Lys Ile Pro His  
385 390 395 400

Leu Lys Asp Asp Lys Pro Gln Ile Leu Ile Ser Ile Gly Asp Ile Ala  
405 410 415

Tyr Glu Val Gly Pro Asp Ile Ala Pro Tyr Val Lys Gln Ile Leu Asp  
420 425 430

Tyr Ile Glu His Asp Leu Gln Thr Lys Phe Lys Phe Arg Lys Lys Phe  
435 440 445

Glu Asn Glu Ile Phe Tyr Cys Ile Gly Arg Leu Ala Val Pro Leu Gly  
450 455 460

Pro Val Leu Gly Lys Leu Leu Asn Arg Asn Ile Leu Asp Leu Met Phe  
465 470 475 480

Lys Cys Pro Leu Ser Asp Tyr Met Gln Glu Thr Phe Gln Ile Leu Thr  
485 490 495

Glu Arg Ile Pro Ser Leu Gly Pro Lys Ile Asn Asp Glu Leu Leu Asn  
500 505 510

Leu Val Cys Ser Thr Leu Ser Gly Thr Pro Phe Ile Gln Pro Gly Ser  
515 520 525

Pro Met Glu Ile Pro Ser Phe Ser Arg Glu Arg Ala Arg Glu Trp Arg  
530 535 540

Asn Lys Ser Ile Leu Gln Lys Thr Gly Glu Ser Asn Asp Asp Asn Asn  
545 550 555 560

Asp Ile Lys Ile Ile Ile Gln Ala Phe Arg Met Leu Lys Asn Ile Lys  
565 570 575

Ser Arg Phe Ser Leu Val Glu Phe Val Arg Ile Val Ala Leu Ser Tyr  
580 585 590

Ile Glu His Thr Asp Pro Arg Val Arg Lys Leu Ala Ala Leu Thr Ser  
595 600 605

Cys Glu Ile Tyr Val Lys Asp Asn Ile Cys Lys Gln Thr Ser Leu His

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610	615	620
Ser Leu Asn Thr Val Ser Glu Val Leu Ser Lys Leu Leu Ala Ile Thr		
625	630	635
Ile Ala Asp Pro Leu Gln Asp Ile Arg Leu Glu Val Leu Lys Asn Leu		
645	650	655
Asn Pro Cys Phe Asp Pro Gln Leu Ala Gln Pro Asp Asn Leu Arg Leu		
660	665	670
Leu Phe Thr Ala Leu His Asp Glu Ser Phe Asn Ile Gln Ser Val Ala		
675	680	685
Met Glu Leu Val Gly Arg Leu Ser Ser Val Asn Pro Ala Tyr Val Ile		
690	695	700
Pro Ser Ile Arg Lys Ile Leu Leu Glu Leu Leu Thr Lys Leu Lys Phe		
705	710	715
Ser Thr Ser Ser Arg Glu Lys Glu Glu Thr Ala Ser Leu Leu Cys Thr		
725	730	735
Leu Ile Arg Ser Ser Lys Asp Val Ala Lys Pro Tyr Ile Glu Pro Leu		
740	745	750
Leu Asn Val Leu Leu Pro Lys Phe Gln Asp Thr Ser Ser Thr Val Ala		
755	760	765
Ser Thr Ala Leu Arg Thr Ile Gly Glu Leu Ser Val Val Gly Gly Glu		
770	775	780
Asp Met Lys Ile Tyr Leu Lys Asp Leu Phe Pro Leu Ile Ile Lys Thr		
785	790	795
Phe Gln Asp Gln Ser Asn Ser Phe Lys Arg Glu Ala Ala Leu Lys Ala		
805	810	815
Leu Gly Gln Leu Ala Ala Ser Ser Gly Tyr Val Ile Asp Pro Leu Leu		
820	825	830
Asp Tyr Pro Glu Leu Leu Gly Ile Leu Val Asn Ile Leu Lys Thr Glu		
835	840	845
Asn Ser Gln Asn Ile Arg Arg Gln Thr Val Thr Leu Ile Gly Ile Leu		
850	855	860
Gly Ala Ile Asp Pro Tyr Arg Gln Lys Glu Arg Glu Val Thr Ser Thr		
865	870	875
880		
Thr Asp Ile Ser Thr Glu Gln Asn Ala Pro Pro Ile Asp Ile Ala Leu		
885	890	895
Leu Met Gln Gly Met Ser Pro Ser Asn Asp Glu Tyr Tyr Thr Thr Val		
900	905	910
Val Ile His Cys Leu Leu Lys Ile Leu Lys Asp Pro Ser Leu Ser Ser		
915	920	925
Tyr His Thr Ala Val Ile Gln Ala Ile Met His Ile Phe Gln Thr Leu		
930	935	940
Gly Leu Lys Cys Val Ser Phe Leu Asp Gln Ile Ile Pro Thr Ile Leu		
945	950	955
960		
Asp Val Met Arg Thr Cys Ser Gln Ser Leu Leu Glu Phe Tyr Phe Gln		
965	970	975
Gln Leu Cys Ser Leu Ile Ile Ile Val Arg Gln His Ile Arg Pro His		
980	985	990
Val Asp Ser Ile Phe Gln Ala Ile Lys Asp Phe Ser Ser Val Ala Lys		
995	1000	1005
Leu Gln Ile Thr Leu Val Ser Val Ile Glu Ala Ile Ser Lys Ala Leu		
1010	1015	1020
Glu Gly Glu Phe Lys Arg Leu Val Pro Leu Thr Leu Thr Leu Phe Leu		
1025	1030	1035
1040		

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Val Ile Leu Glu Asn Asp Lys Ser Ser Asp Lys Val Leu Ser Arg Arg  
1045 1050 1055

Val Leu Arg Leu Leu Glu Ser Phe Gly Pro Asn Leu Glu Gly Tyr Ser  
1060 1065 1070

His Leu Ile Thr Pro Lys Ile Val Gln Met Ala Glu Phe Thr Ser Gly  
1075 1080 1085

Asn Leu Gln Arg Ser Ala Ile Ile Thr Ile Gly Lys Leu Ala Lys Asp  
1090 1095 1100

Val Asp Leu Phe Glu Met Ser Ser Arg Ile Val His Ser Leu Leu Arg  
1105 1110 1115 1120

Val Leu Ser Ser Thr Thr Ser Asp Glu Leu Ser Lys Val Ile Met Asn  
1125 1130 1135

Thr Leu Ser Leu Leu Ile Gln Met Gly Thr Ser Phe Ala Ile Phe  
1140 1145 1150

Ile Pro Val Ile Asn Glu Val Leu Met Lys Lys His Ile Gln His Thr  
1155 1160 1165

Ile Tyr Asp Asp Leu Thr Asn Arg Ile Leu Asn Asn Asp Val Leu Pro  
1170 1175 1180

Thr Lys Ile Leu Glu Ala Asn Thr Thr Asp Tyr Lys Pro Ala Glu Gln  
1185 1190 1195 1200

Met Glu Ala Ala Asp Ala Gly Val Ala Lys Leu Pro Ile Asn Gln Ser  
1205 1210 1215

Val Leu Lys Ser Ala Trp Asn Ser Ser Gln Gln Arg Thr Lys Glu Asp  
1220 1225 1230

Trp Gln Glu Trp Ser Lys Arg Leu Ser Ile Gln Leu Leu Lys Glu Ser  
1235 1240 1245

Pro Ser His Ala Leu Arg Ala Cys Ser Asn Leu Ala Ser Met Tyr Tyr  
1250 1255 1260

Pro Leu Ala Lys Glu Leu Phe Asn Thr Ala Phe Ala Cys Val Trp Thr  
1265 1270 1275 1280

Glu Leu Tyr Ser Gln Tyr Gln Glu Asp Leu Ile Gly Ser Leu Cys Ile  
1285 1290 1295

Ala Leu Ser Ser Pro Leu Asn Pro Pro Glu Ile His Gln Thr Leu Leu  
1300 1305 1310

Asn Leu Val Glu Phe Met Glu His Asp Asp Lys Ala Leu Pro Ile Pro  
1315 1320 1325

Thr Gln Ser Leu Gly Glu Tyr Ala Glu Arg Cys His Ala Tyr Ala Lys  
1330 1335 1340

Ala Leu His Tyr Lys Glu Ile Lys Phe Ile Lys Glu Pro Glu Asn Ser  
1345 1350 1355 1360

Thr Ile Glu Ser Leu Ile Ser Ile Asn Asn Gln Leu Asn Gln Thr Asp  
1365 1370 1375

Ala Ala Ile Gly Ile Leu Lys His Ala Gln Gln His His Ser Leu Gln  
1380 1385 1390

Leu Lys Glu Thr Trp Phe Glu Lys Leu Glu Arg Trp Glu Asp Ala Leu  
1395 1400 1405

His Ala Tyr Asn Glu Arg Glu Lys Ala Gly Asp Thr Ser Val Ser Val  
1410 1415 1420

Thr Leu Gly Lys Met Arg Ser Leu His Ala Leu Gly Glu Trp Glu Gln  
1425 1430 1435 1440

Leu Ser Gln Leu Ala Ala Arg Lys Trp Lys Val Ser Lys Leu Gln Thr  
1445 1450 1455

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Lys Lys Leu Ile Ala Pro Leu Ala Ala Gly Ala Arg Trp Gly Leu Gly  
1460 1465 1470

Glu Trp Asp Met Leu Glu Gln Tyr Ile Ser Val Met Lys Pro Lys Ser  
1475 1480 1485

Pro Asp Lys Glu Phe Phe Asp Ala Ile Leu Tyr Leu His Lys Asn Asp  
1490 1495 1500

Tyr Asp Asn Ala Ser Lys His Ile Leu Asn Ala Arg Asp Leu Leu Val  
1505 1510 1515 1520

Thr Glu Ile Ser Ala Leu Ile Asn Glu Ser Tyr Asn Arg Ala Tyr Ser  
1525 1530 1535

Val Ile Val Arg Thr Gln Ile Ile Thr Glu Phe Glu Glu Ile Ile Lys  
1540 1545 1550

Tyr Lys Gln Leu Pro Pro Asn Ser Glu Lys Lys Leu His Tyr Gln Asn  
1555 1560 1565

Leu Trp Thr Lys Arg Leu Leu Gly Cys Gln Lys Asn Val Asp Leu Trp  
1570 1575 1580

Gln Arg Val Leu Arg Val Arg Ser Leu Val Ile Lys Pro Lys Gln Asp  
1585 1590 1595 1600

Leu Gln Ile Trp Ile Lys Phe Ala Asn Leu Cys Arg Lys Ser Gly Arg  
1605 1610 1615

Met Arg Leu Ala Asn Lys Ala Leu Asn Met Leu Leu Glu Gly Gly Asn  
1620 1625 1630

Asp Pro Ser Leu Pro Asn Thr Val Lys Ala Pro Pro Val Val Tyr  
1635 1640 1645 ,

Ala Gln Leu Lys Tyr Ile Trp Ala Thr Gly Ala Tyr Lys Glu Ala Leu  
1650 1655 1660

Asn His Leu Ile Gly Phe Thr Ser Arg Leu Ala His Asp Leu Gly Leu  
1665 1670 1675 1680

Asp Pro Asn Asn Met Ile Ala Gln Ser Val Lys Leu Ser Ser Ala Ser  
1685 1690 1695

Thr Ala Pro Tyr Val Glu Glu Tyr Thr Lys Leu Leu Ala Arg Cys Phe  
1700 1705 1710

Leu Lys Gln Gly Glu Trp Arg Ile Ala Thr Gln Pro Asn Trp Arg Asn  
1715 1720 1725

Thr Asn Pro Asp Ala Ile Leu Gly Ser Tyr Leu Leu Ala Thr His Phe  
1730 1735 1740

Asp Lys Asn Trp Tyr Lys Ala Trp His Asn Trp Ala Leu Ala Asn Phe  
1745 1750 1755 1760

Glu Val Ile Ser Met Val Gln Glu Glu Thr Lys Leu Asn Gly Gly Lys  
1765 1770 1775

Asn Asp Asp Asp Asp Asp Thr Ala Val Asn Asn Asp Asn Val Arg Ile  
1780 1785 1790

Asp Gly Ser Ile Leu Gly Ser Gly Ser Leu Thr Ile Asn Gly Asn Arg  
1795 1800 1805

Tyr Pro Leu Glu Leu Ile Gln Arg His Val Val Pro Ala Ile Lys Gly  
1810 1815 1820

Phe Phe His Ser Ile Ser Leu Leu Glu Thr Ser Cys Leu Gln Asp Thr  
1825 1830 1835 1840

Leu Arg Leu Leu Thr Leu Leu Phe Asn Phe Gly Gly Ile Lys Glu Val  
1845 1850 1855

Ser Gln Ala Met Tyr Glu Gly Phe Asn Leu Met Lys Ile Glu Asn Trp  
1860 1865 1870

Leu Glu Val Leu Pro Gln Leu Ile Ser Arg Ile His Gln Pro Asp Pro

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1875	1880	1885
Thr Val Ser Asn Ser Leu Leu Ser Leu Leu Ser Asp Leu Gly Lys Ala 1890 1895 1900		
His Pro Gln Ala Leu Val Tyr Pro Leu Thr Val Ala Ile Lys Ser Glu 1905 1910 1915 1920		
Ser Val Ser Arg Gln Lys Ala Ala Leu Ser Ile Ile Glu Lys Ile Arg 1925 1930 1935		
Ile His Ser Pro Val Leu Val Asn Gln Ala Glu Leu Val Ser His Glu 1940 1945 1950		
Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp Tyr Glu Gly Leu 1955 1960 1965		
Glu Asp Ala Arg Arg Gln Phe Phe Val Glu His Asn Ile Glu Lys Met 1970 1975 1980		
Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly Asn Glu Pro Gln 1985 1990 1995 2000		
Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly Arg Asp Leu Asn 2005 2010 2015		
Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Ser Lys Asp Ile Asn 2020 2025 2030		
Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val Phe Arg Lys Ile 2035 2040 2045		
Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu Gln His Val Ser 2050 2055 2060		
Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala Val Pro Gly Thr 2065 2070 2075 2080		
Tyr Phe Pro Gly Lys Pro Thr Ile Arg Ile Ala Lys Phe Glu Pro Leu 2085 2090 2095		
Phe Ser Val Ile Ser Ser Lys Gln Arg Pro Arg Lys Phe Ser Ile Lys 2100 2105 2110		
Gly Ser Asp Gly Lys Asp Tyr Lys Tyr Val Leu Lys Gly His Glu Asp 2115 2120 2125		
Ile Arg Gln Asp Ser Leu Val Met Gln Leu Phe Gly Leu Val Asn Thr 2130 2135 2140		
Leu Leu Lys Asn Asp Ser Glu Cys Phe Lys Arg His Leu Asp Ile Gln 2145 2150 2155 2160		
Gln Tyr Pro Ala Ile Pro Leu Ser Pro Lys Ser Gly Leu Leu Gly Trp 2165 2170 2175		
Val Pro Asn Ser Asp Thr Phe His Val Leu Ile Arg Glu His Arg Asp 2180 2185 2190		
Ala Lys Lys Ile Pro Leu Asn Ile Glu Gln Trp Val Met Leu Gln Met 2195 2200 2205		
Ala Pro Asp Tyr Glu Asn Leu Thr Leu Leu Gln Lys Ile Glu Val Phe 2210 2215 2220		
Thr Tyr Ala Leu Asp Asn Thr Lys Gly Gln Asp Leu Tyr Lys Ile Leu 2225 2230 2235 2240		
Trp Leu Lys Ser Arg Ser Ser Glu Thr Trp Leu Glu Arg Arg Thr Thr 2245 2250 2255		
Tyr Thr Arg Ser Leu Ala Val Met Ser Met Thr Gly Tyr Ile Leu Gly 2260 2265 2270		
Leu Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly 2275 2280 2285		
Lys Val Ile His Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu 2290 2295 2300		

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Arg Glu Lys Tyr Pro Glu Lys Val Pro Phe Arg Leu Thr Arg Met Leu  
2305 2310 2315 2320

Thr Tyr Ala Met Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr  
2325 2330 2335

Cys Glu Asn Val Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met  
2340 2345 2350

Ala Ile Leu Glu Ala Phe Ala Leu Asp Pro Leu Ile His Trp Gly Phe  
2355 2360 2365

Asp Leu Pro Pro Gln Lys Leu Thr Glu Gln Thr Gly Ile Pro Leu Pro  
2370 2375 2380

Leu Ile Asn Pro Ser Glu Leu Leu Arg Lys Gly Ala Ile Thr Val Glu  
2385 2390 2395 2400

Glu Ala Ala Asn Met Glu Ala Glu Gln Asn Glu Thr Arg Asn Ala  
2405 2410 2415

Arg Ala Met Leu Val Leu Arg Arg Ile Thr Asp Lys Leu Thr Gly Asn  
2420 2425 2430

Asp Ile Lys Arg Phe Asn Glu Leu Asp Val Pro Glu Gln Val Asp Lys  
2435 2440 2445

Leu Ile Gln Gln Ala Thr Ser Ile Glu Arg Leu Cys Gln His Tyr Ile  
2450 2455 2460

Gly Trp Cys Pro Phe Trp  
2465 2470

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2474 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Lys Tyr Ile Asn Lys Tyr Thr Thr Pro Pro Asn Leu Leu Ser  
1 5 10 15

Leu Arg Gln Arg Ala Glu Gly Lys His Arg Thr Arg Lys Lys Leu Thr  
20 25 30

His Lys Ser His Ser His Asp Asp Glu Met Ser Thr Thr Ser Asn Thr  
35 40 45

Asp Ser Asn His Asn Gly Pro Asn Asp Ser Gly Arg Val Ile Thr Gly  
50 55 60

Ser Ala Gly His Ile Gly Lys Ile Ser Phe Val Asp Ser Glu Leu Asp  
65 70 75 80

Thr Thr Phe Ser Thr Leu Asn Leu Ile Phe Asp Lys Leu Lys Ser Asp  
85 90 95

Val Pro Gln Glu Arg Ala Ser Gly Ala Asn Glu Leu Ser Thr Thr Leu  
100 105 110

Thr Ser Leu Ala Arg Glu Val Ser Ala Glu Gln Phe Gln Arg Phe Ser  
115 120 125

Asn Ser Leu Asn Asn Lys Ile Phe Glu Leu Ile His Gly Phe Thr Ser  
130 135 140

Ser Glu Lys Ile Gly Gly Ile Leu Ala Val Asp Thr Leu Ile Ser Phe  
145 150 155 160

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**51****52****-continued**


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Tyr Leu Ser Thr Glu Glu Leu Pro Asn Gln Thr Ser Arg Leu Ala Asn  
165 170 175

Tyr Leu Arg Val Leu Ile Pro Ser Ser Asp Ile Glu Val Met Arg Leu  
180 185 190

Ala Ala Asn Thr Leu Gly Arg Leu Thr Val Pro Gly Gly Thr Leu Thr  
195 200 205

Ser Asp Phe Val Glu Phe Glu Val Arg Thr Cys Ile Asp Trp Leu Thr  
210 215 220

Leu Thr Ala Asp Asn Asn Ser Ser Ser Lys Leu Glu Tyr Arg Arg  
225 230 235 240

His Ala Ala Leu Leu Ile Lys Ala Leu Ala Asp Asn Ser Pro Tyr  
245 250 255

Leu Leu Tyr Pro Tyr Val Asn Ser Ile Leu Asp Asn Ile Trp Val Pro  
260 265 270

Leu Arg Asp Ala Lys Leu Ile Ile Arg Leu Asp Ala Ala Val Ala Leu  
275 280 285

Gly Lys Cys Leu Thr Ile Ile Gln Asp Arg Asp Pro Ala Leu Gly Lys  
290 295 300

Gln Trp Phe Gln Arg Leu Phe Gln Gly Cys Thr His Gly Leu Ser Leu  
305 310 315 320

Asn Thr Asn Asp Ser Val His Ala Thr Leu Leu Val Phe Arg Glu Leu  
325 330 335

Leu Ser Leu Lys Ala Pro Tyr Leu Arg Asp Lys Tyr Asp Asp Ile Tyr  
340 345 350

Lys Ser Thr Met Lys Tyr Lys Glu Tyr Lys Phe Asp Val Ile Arg Arg  
355 360 365

Glu Val Tyr Ala Ile Leu Pro Leu Leu Ala Ala Phe Asp Pro Ala Ile  
370 375 380

Phe Thr Lys Lys Tyr Leu Asp Arg Ile Met Val His Tyr Leu Arg Tyr  
385 390 395 400

Leu Lys Asn Ile Asp Met Asn Ala Ala Asn Asn Ser Asp Lys Pro Phe  
405 410 415

Ile Leu Val Ser Ile Gly Asp Ile Ala Phe Glu Val Gly Ser Ser Ile  
420 425 430

Ser Pro Tyr Met Thr Leu Ile Leu Asp Asn Ile Arg Glu Gly Leu Arg  
435 440 445

Thr Lys Phe Lys Val Arg Lys Gln Phe Glu Lys Asp Leu Phe Tyr Cys  
450 455 460

Ile Gly Lys Leu Ala Cys Ala Leu Gly Pro Ala Phe Ala Lys His Leu  
465 470 475 480

Asn Lys Asp Leu Leu Asn Leu Met Leu Asn Cys Pro Met Ser Asp His  
485 490 495

Met Gln Glu Thr Leu Met Ile Leu Asn Glu Lys Ile Pro Ser Leu Glu  
500 505 510

Ser Thr Val Asn Ser Arg Ile Leu Asn Leu Leu Ser Ile Ser Leu Ser  
515 520 525

Gly Glu Lys Phe Ile Gln Ser Asn Gln Tyr Asp Phe Asn Asn Gln Phe  
530 535 540

Ser Ile Glu Lys Ala Arg Lys Ser Arg Asn Gln Ser Phe Met Lys Lys  
545 550 555 560

Thr Gly Glu Ser Asn Asp Asp Ile Thr Asp Ala Gln Ile Leu Ile Gln  
565 570 575

Cys Phe Lys Met Leu Gln Leu Ile His His Gln Tyr Ser Leu Thr Glu

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-continued

580	585	590
Phe Val Arg Leu Ile Thr Ile Ser Tyr Ile Glu His Glu Asp Ser Ser		
595	600	605
Val Arg Lys Leu Ala Ala Leu Thr Ser Cys Asp Leu Phe Ile Lys Asp		
610	615	620
Asp Ile Cys Lys Gln Thr Ser Val His Ala Leu His Ser Val Ser Glu		
625	630	635
640		
Val Leu Ser Lys Leu Leu Met Ile Ala Ile Thr Asp Pro Val Ala Glu		
645	650	655
Ile Arg Leu Glu Ile Leu Gln His Leu Gly Ser Asn Phe Asp Pro Gln		
660	665	670
Leu Ala Gln Pro Asp Asn Leu Arg Leu Leu Phe Met Ala Leu Asn Asp		
675	680	685
Glu Ile Phe Gly Ile Gln Leu Glu Ala Ile Lys Ile Ile Gly Arg Leu		
690	695	700
Ser Ser Val Asn Pro Ala Tyr Val Val Pro Ser Leu Arg Lys Thr Leu		
705	710	715
720		
Leu Glu Leu Leu Thr Gln Leu Lys Phe Ser Asn Met Pro Lys Lys Lys		
725	730	735
Glu Glu Ser Ala Thr Leu Leu Cys Thr Leu Ile Asn Ser Ser Asp Glu		
740	745	750
Val Ala Lys Pro Tyr Ile Asp Pro Ile Leu Asp Val Ile Leu Pro Lys		
755	760	765
Cys Gln Asp Ala Ser Ser Ala Val Ala Ser Thr Ala Leu Lys Val Leu		
770	775	780
Gly Glu Leu Ser Val Val Gly Gly Lys Glu Met Thr Arg Tyr Leu Lys		
785	790	795
800		
Glu Leu Met Pro Leu Ile Ile Asn Thr Phe Gln Asp Gln Ser Asn Ser		
805	810	815
Phe Lys Arg Asp Ala Ala Leu Thr Thr Leu Gly Gln Leu Ala Ala Ser		
820	825	830
Ser Gly Tyr Val Val Gly Pro Leu Leu Asp Tyr Pro Glu Leu Leu Gly		
835	840	845
Ile Leu Ile Asn Ile Leu Lys Thr Glu Asn Asn Pro His Ile Arg Arg		
850	855	860
Gly Thr Val Arg Leu Ile Gly Ile Leu Gly Ala Leu Asp Pro Tyr Lys		
865	870	875
880		
His Arg Glu Ile Glu Val Thr Ser Asn Ser Lys Ser Ser Val Glu Gln		
885	890	895
Asn Ala Pro Ser Ile Asp Ile Ala Leu Leu Met Gln Gly Val Ser Pro		
900	905	910
Ser Asn Asp Glu Tyr Tyr Pro Thr Val Val Ile His Asn Leu Met Lys		
915	920	925
Ile Leu Asn Asp Pro Ser Leu Ser Ile His His Thr Ala Ala Ile Gln		
930	935	940
Ala Ile Met His Ile Phe Gln Asn Leu Gly Leu Arg Cys Val Ser Phe		
945	950	955
960		
Leu Asp Gln Ile Ile Pro Gly Ile Ile Leu Val Met Arg Ser Cys Pro		
965	970	975
Pro Ser Gln Leu Asp Phe Tyr Phe Gln Gln Leu Gly Ser Leu Ile Ser		
980	985	990
Ile Val Lys Gln His Ile Arg Pro His Val Glu Lys Ile Tyr Gly Val		
995	1000	1005

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**55****56****-continued**


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Ile Arg Glu Phe Phe Pro Ile Ile Lys Leu Gln Ile Thr Ile Ile Ser  
1010 1015 1020

Val Ile Glu Ser Ile Ser Lys Ala Leu Glu Gly Glu Phe Lys Arg Phe  
1025 1030 1035 1040

Val Pro Glu Thr Leu Thr Phe Phe Leu Asp Ile Leu Glu Asn Asp Gln  
1045 1050 1055

Ser Asn Lys Arg Ile Val Pro Ile Arg Ile Leu Lys Ser Leu Val Thr  
1060 1065 1070

Phe Gly Pro Asn Leu Glu Asp Tyr Ser His Leu Ile Met Pro Ile Val  
1075 1080 1085

Val Arg Met Thr Glu Tyr Ser Ala Gly Ser Leu Lys Lys Ile Ser Ile  
1090 1095 1100

Ile Thr Leu Gly Arg Leu Ala Lys Asn Ile Asn Leu Ser Glu Met Ser  
1105 1110 1115 1120

Ser Arg Ile Val Gln Ala Leu Val Arg Ile Leu Asn Asn Gly Asp Arg  
1125 1130 1135

Glu Leu Thr Lys Ala Thr Met Asn Thr Leu Ser Leu Leu Leu Gln  
1140 1145 1150

Leu Gly Thr Asp Phe Val Val Phe Val Pro Val Ile Asn Lys Ala Leu  
1155 1160 1165

Leu Arg Asn Arg Ile Gln His Ser Val Tyr Asp Gln Leu Val Asn Lys  
1170 1175 1180

Leu Leu Asn Asn Glu Cys Leu Pro Thr Asn Ile Ile Phe Asp Lys Glu  
1185 1190 1195 1200

Asn Glu Val Pro Glu Arg Lys Asn Tyr Glu Asp Glu Met Gln Val Thr  
1205 1210 1215

Lys Leu Pro Val Asn Gln Asn Ile Leu Lys Asn Ala Trp Tyr Cys Ser  
1220 1225 1230

Gln Gln Lys Thr Lys Glu Asp Trp Gln Glu Trp Ile Arg Arg Leu Ser  
1235 1240 1245

Ile Gln Leu Leu Lys Glu Ser Pro Ser Ala Cys Leu Arg Ser Cys Ser  
1250 1255 1260

Ser Leu Val Ser Val Tyr Tyr Pro Leu Ala Arg Glu Leu Phe Asn Ala  
1265 1270 1275 1280

Ser Phe Ser Ser Cys Trp Val Glu Leu Gln Thr Ser Tyr Gln Glu Asp  
1285 1290 1295

Leu Ile Gln Ala Leu Cys Lys Ala Leu Ser Ser Ser Glu Asn Pro Pro  
1300 1305 1310

Glu Ile Tyr Gln Met Leu Leu Asn Leu Val Glu Phe Met Glu His Asp  
1315 1320 1325

Asp Lys Pro Leu Pro Ile Pro Ile His Thr Leu Gly Lys Tyr Ala Gln  
1330 1335 1340

Lys Cys His Ala Phe Ala Lys Ala Leu His Tyr Lys Glu Val Glu Phe  
1345 1350 1355 1360

Leu Glu Glu Pro Lys Asn Ser Thr Ile Glu Ala Leu Ile Ser Ile Asn  
1365 1370 1375

Asn Gln Leu His Gln Thr Asp Ser Ala Ile Gly Ile Leu Lys His Ala  
1380 1385 1390

Gln Gln His Asn Glu Leu Gln Leu Lys Glu Thr Trp Tyr Glu Lys Leu  
1395 1400 1405

Gln Arg Trp Glu Asp Ala Leu Ala Ala Tyr Asn Glu Lys Glu Ala Ala  
1410 1415 1420

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-continued

Gly Glu Asp Ser Val Val Glu Val Met Met Gly Lys Leu Arg Ser Leu Tyr  
 1425 1430 1435 1440

Ala Leu Gly Glu Trp Glu Glu Leu Ser Lys Leu Ala Ser Glu Lys Trp  
 1445 1450 1455

Gly Thr Ala Lys Pro Glu Val Lys Lys Ala Met Ala Pro Leu Ala Ala  
 1460 1465 1470

Gly Ala Ala Trp Gly Leu Glu Gln Trp Asp Glu Ile Ala Gln Tyr Thr  
 1475 1480 1485

Ser Val Met Lys Ser Gln Ser Pro Asp Lys Glu Phe Tyr Asp Ala Ile  
 1490 1495 1500

Leu Cys Leu His Arg Asn Asn Phe Lys Lys Ala Glu Val His Ile Phe  
 1505 1510 1515 1520

Asn Ala Arg Asp Leu Leu Val Thr Glu Leu Ser Ala Leu Val Asn Glu  
 1525 1530 1535

Ser Tyr Asn Arg Ala Tyr Asn Val Val Val Arg Ala Gln Ile Ile Ala  
 1540 1545 1550

Glu Leu Glu Glu Ile Ile Lys Tyr Lys Lys Leu Pro Gln Asn Ser Asp  
 1555 1560 1565

Lys Arg Leu Thr Met Arg Glu Thr Trp Asn Thr Arg Leu Leu Gly Cys  
 1570 1575 1580

Gln Lys Asn Ile Asp Val Trp Gln Arg Ile Leu Arg Val Arg Ser Leu  
 1585 1590 1595 1600

Val Ile Lys Pro Lys Glu Asp Ala Gln Val Arg Ile Lys Phe Ala Asn  
 1605 1610 1615

Leu Cys Arg Lys Ser Gly Arg Met Ala Leu Ala Lys Lys Val Leu Asn  
 1620 1625 1630

Thr Leu Leu Glu Glu Thr Asp Asp Pro Asp His Pro Asn Thr Ala Lys  
 1635 1640 1645

Ala Ser Pro Pro Val Val Tyr Ala Gln Leu Lys Tyr Leu Trp Ala Thr  
 1650 1655 1660

Gly Leu Gln Asp Glu Ala Leu Lys Gln Leu Ile Asn Phe Thr Ser Arg  
 1665 1670 1675 1680

Met Ala His Asp Leu Gly Leu Asp Pro Asn Asn Met Ile Ala Gln Ser  
 1685 1690 1695

Val Pro Gln Gln Ser Lys Arg Val Pro Arg His Val Glu Asp Tyr Thr  
 1700 1705 1710

Lys Leu Leu Ala Arg Cys Phe Leu Lys Gln Gly Glu Trp Arg Val Cys  
 1715 1720 1725

Leu Gln Pro Lys Trp Arg Leu Ser Asn Pro Asp Ser Ile Leu Gly Ser  
 1730 1735 1740

Tyr Leu Leu Ala Thr His Phe Asp Asn Thr Trp Tyr Lys Ala Trp His  
 1745 1750 1755 1760

Asn Trp Ala Leu Ala Asn Phe Glu Val Ile Ser Met Leu Thr Ser Val  
 1765 1770 1775

Ser Lys Lys Gln Glu Gly Ser Asp Ala Ser Ser Val Thr Asp Ile  
 1780 1785 1790

Asn Glu Phe Asp Asn Gly Met Ile Gly Val Asn Thr Phe Asp Ala Lys  
 1795 1800 1805

Glu Val His Tyr Ser Ser Asn Leu Ile His Arg His Val Ile Pro Ala  
 1810 1815 1820

Ile Lys Gly Phe Phe His Ser Ile Ser Leu Ser Glu Ser Ser Ser Leu  
 1825 1830 1835 1840

Gln Asp Ala Leu Arg Leu Leu Thr Leu Trp Phe Thr Phe Gly Gly Ile

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**59****60****-continued**

1845	1850	1855
Pro Glu Ala Thr Gln Ala Met His	Glu Gly Phe Asn Leu Ile Gln Ile	
1860	1865	1870
Gly Thr Trp Leu Glu Val Leu Pro Gln Leu Ile Ser Arg Ile His Gln		
1875	1880	1885
Pro Asn Gln Ile Val Ser Arg Ser Leu Leu Ser Leu Leu Ser Asp Leu		
1890	1895	1900
Gly Lys Ala His Pro Gln Ala Leu Val Tyr Pro Leu Met Val Ala Ile		
1905	1910	1915
Lys Ser Glu Ser Leu Ser Arg Gln Lys Ala Ala Leu Ser Ile Ile Glu		
1925	1930	1935
Lys Met Arg Ile His Ser Pro Val Leu Val Asp Gln Ala Glu Leu Val		
1940	1945	1950
Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp Tyr		
1955	1960	1965
Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn Thr		
1970	1975	1980
Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys Arg		
1985	1990	1995
Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly Arg		
2005	2010	2015
Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser Lys		
2020	2025	2030
Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val Phe		
2035	2040	2045
Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu Gln		
2050	2055	2060
His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala Val		
2065	2070	2075
Pro Gly Thr Arg Ala Ser Gly Gly Lys Pro Ile Val Lys Ile Ser Lys		
2085	2090	2095
Phe Glu Pro Val Phe Ser Val Ile Ser Ser Lys Gln Arg Pro Arg Lys		
2100	2105	2110
Phe Cys Ile Lys Gly Ser Asp Gly Lys Asp Tyr Lys Tyr Val Leu Lys		
2115	2120	2125
Gly His Glu Asp Ile Arg Gln Asp Ser Leu Val Met Gln Leu Phe Gly		
2130	2135	2140
Leu Val Asn Thr Leu Leu Gln Asn Asp Ala Glu Cys Phe Arg Arg His		
2145	2150	2155
Leu Asp Ile Gln Gln Tyr Pro Ala Ile Pro Leu Ser Pro Lys Ser Gly		
2165	2170	2175
Leu Leu Gly Trp Val Pro Asn Ser Asp Thr Phe His Val Leu Ile Arg		
2180	2185	2190
Glu His Arg Glu Ala Lys Lys Ile Pro Leu Asn Ile Glu His Trp Val		
2195	2200	2205
Met Leu Gln Met Ala Pro Asp Tyr Asp Asn Leu Thr Leu Leu Gln Lys		
2210	2215	2220
Val Glu Val Phe Thr Tyr Ala Leu Asn Asn Thr Glu Gly Gln Asp Leu		
2225	2230	2235
Tyr Lys Val Leu Trp Leu Lys Ser Arg Ser Ser Glu Thr Trp Leu Glu		
2245	2250	2255
Arg Arg Thr Thr Tyr Thr Arg Ser Leu Ala Val Met Ser Met Thr Gly		
2260	2265	2270

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**61****62****-continued**

Tyr Ile Leu Gly Leu Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp  
2275 2280 2285

Arg Ile Thr Gly Lys Val Ile His Ile Asp Phe Gly Asp Cys Phe Glu  
2290 2295 2300

Ala Ala Ile Leu Arg Glu Phe Pro Glu Lys Val Pro Phe Arg Leu  
2305 2310 2315 2320

Thr Arg Met Leu Thr Tyr Ala Met Glu Val Ser Gly Ile Glu Gly Ser  
2325 2330 2335

Phe Arg Ile Thr Cys Glu Asn Val Met Lys Val Leu Arg Asp Asn Lys  
2340 2345 2350

Gly Ser Leu Met Ala Ile Leu Glu Ala Phe Ala Phe Asp Pro Leu Ile  
2355 2360 2365

Asn Trp Gly Phe Asp Leu Pro Thr Lys Ile Glu Glu Glu Thr Gly  
2370 2375 2380

Ile Gln Leu Pro Val Met Asn Ala Asn Glu Leu Leu Ser Asn Gly Ala  
2385 2390 2395 2400

Ile Thr Glu Glu Val Gln Arg Val Glu Asn Glu His Lys Asn Ala  
2405 2410 2415

Ile Arg Asn Ala Arg Ala Met Leu Val Leu Lys Arg Ile Thr Asp Lys  
2420 2425 2430

Leu Thr Gly Asn Asp Ile Arg Arg Phe Asn Asp Leu Asp Val Pro Glu  
2435 2440 2445

Gln Val Asp Lys Leu Ile Gln Gln Ala Thr Ser Val Glu Asn Leu Cys  
2450 2455 2460

Gln His Tyr Ile Gly Trp Cys Pro Phe Trp  
2465 2470

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGATCCCG TCGAGCTTCA GTTGAAC TAC GGC GTGCTTC TGTAGCCATG GGAGTGCAGG	60
TGGA	64

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCGGAAATT CTCATTCCAG TTTTAGAA	28
--------------------------------	----

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(iii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Tyr Asp Pro Asn Gln Pro  
1 . . . . . 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Ile Asp Phe Gly Asp  
1 . . . . . 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Asp Gln Val Phe Glu  
1 . . . . . 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCCACCA GATTTGCT

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGGATCCCG TCGAGCTTCA GTTGAACTAC GGCGTGCTTC TGTAGCCATG CGGGCGGCCG

60

TTCC

64

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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**65****66****-continued**

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCCGGAATT CTCAATCAAT ATCCACTA

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGGGATCCA CNTAYGAYCC NAAYCARC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGAATTCA TCNCCRAART CDATRTG

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGGGATCCA AYGAYCARGT NTTYGA

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What is claimed is:

1. An isolated, purified cDNA molecule which encodes RAFT1, a protein having the amino acid sequence as shown in SEQ ID NO:2 wherein the acronym RAFT connotes a rapamycin and FKBP12 target.

2. The isolated, purified cDNA molecule of claim 1 which comprises the nucleotide sequence as shown in SEQ ID NO:1, nucleotides 64-7710.

3. An isolated, purified intron-free DNA molecule consisting of at least 20 contiguous nucleotides encoding all or a portion of the amino acid sequence as shown in SEQ ID NO: 2.

4. An isolated, purified intron-free DNA molecule consisting of at least 20 contiguous nucleotides of the sequence as shown in SEQ ID NO: 1.

5. An isolated DNA molecule encoding a rat RAFT protein obtained by a method comprising the steps of:

(a) probing a library of rat cDNA sequences with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and

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(b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

6. An isolated DNA molecule encoding a rat RAFT protein obtained by a method comprising the steps of:

(a) amplifying a DNA sequence using (i) at least one primer which comprises at least 10 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1 and (ii) a template which comprises rat cDNA or mRNA; and

(b) isolating an amplified DNA sequence which contains a complete open reading frame encoding a polypeptide of about 2550 amino acids encoding a rat RAFT protein,

65 wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

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7. An isolated DNA molecule encoding a rat RAFT protein identified by a process comprising the steps of:

- (a) annealing a set of mixed oligonucleotides to a rat cDNA library, each member of said set of mixed oligonucleotides encoding a sequence of at least six contiguous amino acids of the amino acid sequence shown in SEQ ID NO:2; and
- (b) isolating a rat cDNA molecule which (i) anneals to at least one member of the set of mixed oligonucleotides, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

8. An isolated DNA molecule encoding a rat RAFT protein according to claim 7, wherein two sets of mixed oligonucleotides are annealed.

9. An isolated DNA molecule having a nucleotide sequence, or a degenerate sequence thereof, obtained by a method comprising the steps of:

- (a) probing a library of rat cDNA molecules with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and
- (b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame

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encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

10. A method of isolating a DNA molecule encoding a mammalian RAFT protein comprising the steps of:

- (a) probing a library of rat cDNA sequences with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and
- (b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

11. The method of claim 10 wherein the probe comprises at least 20 contiguous nucleotides encoding all or a portion of the amino acid sequence as shown in SEQ ID NO:2.

12. The method of claim 10 wherein the probe comprises at least 20 contiguous nucleotides as shown in SEQ ID NO:1.

\* \* \* \* \*

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : 6,492,106 B1  
APPLICATION NO. : 08/305790  
DATED : December 10, 2002  
INVENTOR(S) : David M. Sabatini et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

On Title Page, should read, under (73) Assignee:

--Sloan-Kettering Institute for Cancer Research, New York, NY (US)-- has been inserted.

Signed and Sealed this

Seventeenth Day of October, 2006

A black and white photograph of a handwritten signature. The signature reads "Jon W. Dudas". The "J" is stylized with a long vertical stroke and a small loop at the top. "W." is a simple "W" with a dot over it. "Dudas" is written in a cursive script.

JON W. DUDAS  
*Director of the United States Patent and Trademark Office*